

**In the Specification:**

Please amend the specification as follows:

In the drawings, please substitute the enclosed Replacement Sheets 10/15, 11/15, 12/15, 13/15, 14/15, and 15/15 for the corresponding sheets.

Please delete the paragraph on page 6, lines 33-35, to page and replace it with the following paragraph:

**Fig. 9a-9e:** are illustrations of the results obtained from the >find patterns= program of the GCG sequence analysis package (SEQ ID NOS 20-24, respectively in order of appearance in Figure 9a, SEQ ID NO: 25 in Fig. 9(b), SEQ ID NO: 26 in Fig. 9(c), SEQ ID NO: 27 in Fig. 9(d), and SEQ ID NO: 28 in Fig 9(e)).

Please delete the paragraph starting at page 29, line 18, and replace it with the following paragraph:

**Materials and Methods:**

The sequence of the regulatory region of CYP3A5 was analysed with the 'findpatterns' program of the GCG sequence analysis package (GCG, Madison, Wisconsin). This program finds specific DNA sequence motifs, patterns, and transcription binding sites, whose sequences are stored in the program, and are present in the sequence of interest. In the present analysis, at most one single mismatch or error per pattern is allowed in the sequence of interest, to detect if the two reported variations alter any known motifs or transcription binding sites. Results are identified in Figures 9a to 9e..